

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: Evans, Ronald M.  
No, David

(ii) TITLE OF INVENTION: HORMONE-MEDIATED METHODS FOR MODULATING  
EXPRESSION OF EXOGENOUS GENES IN MAMMALIAN SYSTEMS, AND  
PRODUCTS RELATED THERETO

(iii) NUMBER OF SEQUENCES: 18

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Gray Cary Ware & Freidenrich LLP  
(B) STREET: 4365 Executive Drive, Suite 1600  
(C) CITY: San Diego  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 92121-2189

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/974,530  
(B) FILING DATE: November 19, 1997  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Reiter, Stephen E.  
(B) REGISTRATION NUMBER: 31,192  
(C) REFERENCE/DOCKET NUMBER: SALK1520-2

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 619-677-1409  
(B) TELEFAX: 619-677-1465

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```

Cys Xaa Xaa Cys Xaa Xaa Asp Xaa Ala Xaa Gly Xaa Tyr Xaa Xaa Xaa
1      5      10      15

Xaa Cys Xaa Xaa Cys Lys Xaa Phe Phe Xaa Arg Xaa Xaa Xaa Xaa Xaa
      20      25      30

Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
      35      40      45

Xaa Xaa Xaa Lys Xaa Xaa Arg Xaa Xaa Cys Xaa Xaa Cys Arg Xaa Xaa
      50      55      60

Lys Cys Xaa Xaa Xaa Gly Met
65      70

```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

Glu Gly Cys Lys Gly
1      5

```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gly Ser Cys Lys Val  
1 5

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2241 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 1..2241  
(D) OTHER INFORMATION: /product= "VgEcR"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATG GCC CCG ACC GAT GTC AGC CTG GCG GAC GAG CTC CAC TTA GAC	48
Met Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp	
1 5 10 15	
GCG GAG GAC CTC CCG ATG CCG CAT GCG GAC CCG CTA GAC GAT TTC GAT	96
Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp	
20 25 30	
CTG CAC ATG TTG GCG GAC GGG GAT TCC CCG GGT CCG GGA TTT ACC CCG	144
Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro	
35 40 45	
CAC GAC TCC GCG CCG TAC GCG GCT CTG GAT ATG GCG GAC TTC GAG TTT	192
His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe	
50 55 60	
GAG CAG ATG TTT ACC GAT GCG CTT GGA ATT GAC GAG TAC GGT CCG AAG	240
Glu Glu Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly Lys	
65 70 75 80	
CTT CTA GGT ACC TCT AGA AGC ATA TCG AAT TCT ATA TCT TCA GGT CCG	288
Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg	
85 90 95	
GAT GAT CTC TCG CCT TCG AGC AGC TTG AAC GGA TAC TCG CCG AAC GAA	336
Asp Asp Leu Ser Pro Ser Ser Ser Leu Asn Gly Tyr Ser Ala Asn Glu	
100 105 110	
AGC TCG GAT GCG AAG AAG AGC AAG AAG GGA CTT GCG CCA CCG CTC CAA	384
Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala Pro Arg Val Gln	
115 120 125	

GAG GAG CTC TGC CTC GTT TGC GGC GAC AGG GCC TCC GGC TAC CAC TAC 432  
 Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr  
 130 135 140

AAC GCC CTC ACC TGT CGA TCC TGC AAG CTC TTC TTT CGA CGC AGC GTT 480  
 Asn Ala Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Arg Arg Ser Val  
 145 150 155 160

ACC AAG AGC GCC CTC TAC TGC TGC AAG TTC GGG CGC GCC TGC GAA ATG 528  
 Thr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg Ala Cys Glu Met  
 165 170 175

GAC ATG TAC ATG AGG CGA AAG TGT CAG GAG TGC CGC CTC AAA AAG TGC 576  
 Asp Met Tyr Met Arg Arg Lys Cys Glu Glu Cys Arg Leu Lys Lys Cys  
 180 185 190

CTC GCC CTC GGT ATG CGG CGG GAA TGC CTC CTC CGG GAG AAC CAA TGT 624  
 Leu Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Asn Glu Cys  
 195 200 205

CGC ATG AAG CGC CGC GAA AAG AAG GCC CAG AAG GAG AAG GAC AAA ATG 672  
 Ala Met Lys Arg Arg Glu Lys Lys Ala Glu Lys Glu Lys Asp Lys Met  
 210 215 220

ACC ACT TCC CGC AGC TCT CAG CAT GCC CGC AAT GCC AGC TTG GCC TCT 720  
 Thr Thr Ser Pro Ser Ser Glu His Gly Gly Asn Gly Ser Leu Ala Ser  
 225 230 235 240

GGT GCC GCC CAA GAC TTT GTT AAG AAG GAG ATT CTT GAC CTT ATG ACA 768  
 Gly Gly Gly Glu Asp Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr  
 245 250 255

TGC GAG CGC CGC CAG CAT GCC ACT ATT CGC CTA CTA CCT GAT GAA ATA 816  
 Cys Glu Pro Pro Glu His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile  
 260 265 270

TTG GCC AAG TGT CAA GCC CGC AAT ATA CCT TCC TTA ACG TAC AAT CAG 864  
 Leu Ala Lys Cys Glu Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Glu  
 275 280 285

TTG GCC GTT ATA TAC AAG TTA ATT TGC TAC CAG GAT GCC TAT CAG CAG 912  
 Leu Ala Val Ile Tyr Lys Leu Ile Trp Tyr Glu Asp Gly Tyr Glu Glu  
 290 295 300

CCA TCT GAA GAG GAT CTC AGG CGT ATA ATC AGT CAA CCC GAT CAG AAC 960  
 Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Glu Pro Asp Glu Asn  
 305 310 315 320

GAG AGC CAA ACG GAC GTC AGC TTT CGG CAT ATA ACC GAG ATA ACC ATA 1008  
 Glu Ser Glu Thr Asp Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile  
 325 330 335

CTC ACC CTC CAG TTG ATT GTT GAG TTT GCT AAA GGT CTA CCA GCC TTT 1056  
 Leu Thr Val Glu Leu Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe  
 340 345 350

ACA AAG ATA CCC CAG GAG GAG CAG ATC ACC TTA CTA AAG CCC TCC TCC 1104  
 Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser  
 355 360 365

TCC GAG GTG ATG ATG CTG CGT ATG GCA CGA CCG TAT GAC CAC AGC TCC 1152  
 Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser  
 370 375 380

GAC TCA ATA TTC TTC CCG AAT AAT AGA TCA TAT ACC CCG GAT TCT TAC 1200  
 Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr  
 385 390 395 400

AAA ATG CCC GGA ATG GCT GAT AAC ATT GAA GAC CTG CTG CAT TTC TCC 1248  
 Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys  
 405 410 415

CGC CAA ATG TTC TCC ATG AAG CTG GAC AAC CTC GAA TAC CCG CTT CTC 1296  
 Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu  
 420 425 430

ACT CCC ATT CTG ATC TTC TCC GAC CCG CCG GGC CTG GAG AAG GCC CAA 1344  
 Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Gln  
 435 440 445

CTA CTC GAA CCG ATC CAG AGC TAC TAC ATC CAC ACC CTA CCG ATT TAT 1392  
 Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr  
 450 455 460

ATA CTC AAC CCC CAC TCC GGC GAC TCA ATG AGC CTC CTC TTC TAC GCA 1440  
 Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala  
 465 470 475 480

AAG CTC CTC TCC ATC CTC ACC GAG CTG CCT ACC CTG GGC AAC CAG AAC 1488  
 Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn  
 485 490 495

GCC GAG ATG TGT TTC TCA CTA AAG CTC AAA AAC CCG AAA CTC CCC AAG 1536  
 Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys  
 500 505 510

TTC CTC GAG GAG ATC TCG GAC GTT CAT GCC ATC CCG CCA TCG CTC CAG 1584  
 Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Gln  
 515 520 525

TCC CAC CTT CAG ATT ACC CAG GAG GAG AAC GAG CGT CTC GAG CCG GCT 1632  
 Ser His Leu Gln Ile Thr Gln Glu Glu Asn Glu Arg Leu Glu Arg Ala  
 530 535 540

GAG CGT ATG CCG GCA TCG GTT GGG GGC GCC ATT ACC GCC GCG ATT GAT 1680  
 Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp  
 545 550 555 560

TGC GAC TCT GCC TCC ACT TCC GCG GCG GCA GCC GCG GCC CAG CAT CAG 1728  
 Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala Glu His Gln  
 565 570 575

CCT CAG CCT CAG CCC CAG CCC CAA CCC TCC TCC CTC ACC CAG AAC GAT 1776  
 Pro Gln Pro Gln Pro Gln Pro Gln Pro Ser Ser Leu Thr Gln Asn Asp  
 580 585 590

TCC CAG CAG CAG ACA CAG CCC CAG CTA CAA CCT CAG CTA CCA CCT CAG 1824  
 Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln Leu Pro Pro Gln  
 595 600 605

CTC CAA GGT CAA CTC CAA CCC CAG CTC CAA CCA CAG CTT CAG ACG CAA 1872  
 Leu Gln Gly Gln Leu Gln Pro Gln Leu Gln Pro Gln Leu Gln Thr Gln  
 610 615 620

CTC CAG CCA CAG ATT CAA CCA CAG CCA CAG CTC CTT CCC GTC TCC GCT 1920  
 Leu Gln Pro Gln Ile Gln Pro Gln Pro Gln Leu Leu Pro Val Ser Ala  
 625 630 635 640

CCC GTC CCC CCC TCC CTA ACC GCA CCT GGT TCC TTG TCC CCC GTC AGT 1968  
 Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu Ser Ala Val Ser  
 645 650 655

ACG AGC AGC GAA TAC ATG CCC GGA ACT GCG GCC ATA GGA CCC ATC ACG 2016  
 Thr Ser Ser Gln Tyr Met Gly Gly Ser Ala Ala Ile Gly Pro Ile Thr  
 660 665 670

CCG GCA ACC ACC AGC AGT ATC ACG GCT CCC GTT ACC GCT AGC TCC ACC 2064  
 Pro Ala Thr Thr Ser Ser Ile Thr Ala Ala Val Thr Ala Ser Ser Thr  
 675 680 685

ACA TCA GCG CTA CCG ATG CCC AAC GGA GTT GGA CTC GGT GTT GCG CTC 2112  
 Thr Ser Ala Val Pro Met Gly Asn Gly Val Gly Val Gly Val  
 690 695 700

GGC GGC AAC GTC AGC ATG TAT GCG AAC CCC CAG ACG CCC ATG CCC TTG 2160  
 Gly Gly Asn Val Ser Met Tyr Ala Asn Ala Gln Thr Ala Met Ala Leu  
 705 710 715 720

ATG GGT CTA GCG CTC CAT TCG CAC CAA CAG CAG CTT ATC GCG GGA CTC 2208  
 Met Gly Val Ala Leu His Ser His Gln Gln Gln Leu Ile Gly Gly Val  
 725 730 735

GCG GTT AAG TCG GAG CAC TCG ACG ACT GCA TAG 2241  
 Ala Val Lys Ser Gln His Ser Thr Thr Ala  
 740 745

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 746 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp  
1 5 10 15

Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp  
20 25 30

Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro  
35 40 45

His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe  
50 55 60

Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly Lys  
65 70 75 80

Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg  
85 90 95

Asp Asp Leu Ser Pro Ser Ser Ser Leu Asn Gly Tyr Ser Ala Asn Glu  
100 105 110

Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala Pro Arg Val Gln  
115 120 125

Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr  
130 135 140

Asn Ala Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Arg Arg Ser Val  
145 150 155 160

Thr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg Ala Cys Glu Met  
165 170 175

Asp Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys  
180 185 190

Leu Ala Val Gly Met Arg Pro Gln Cys Val Val Pro Glu Asn Gln Cys  
195 200 205

Ala Met Lys Arg Arg Gln Lys Lys Ala Gln Lys Glu Lys Asp Lys Met  
210 215 220

Thr Thr Ser Pro Ser Ser Gln His Gly Gly Asn Gly Ser Leu Ala Ser  
225 230 235 240

Gly Gly Gly Gln Asp Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr  
245 250 255

Cys Glu Pro Pro Gln His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile  
260 265 270

Leu Ala Lys Cys Gln Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln  
275 280 285

Leu Ala Val Ile Tyr Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln  
290 295 300

Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn  
305 310 315 320

Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile  
325 330 335

Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe  
340 345 350

Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser  
355 360 365

Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser  
370 375 380

Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr  
385 390 395 400

Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys  
405 410 415

Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu  
420 425 430

Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Gln  
435 440 445

Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr  
450 455 460

Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala  
465 470 475 480

Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn  
485 490 495

Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys  
500 505 510

Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Gln  
515 520 525

Ser His Leu Gln Ile Thr Gln Glu Glu Asn Glu Arg Leu Glu Arg Ala  
530 535 540

Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp  
545 550 555 560

Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala Ala Gln His Gln  
565 570 575

Pro Gln Pro Gln Pro Gln Pro Gln Pro Ser Ser Leu Thr Gln Asn Asp  
580 585 590

Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln Leu Pro Pro Gln



595            600            605  
 Leu Gln Gly Gln Leu Gln Pro Gln Leu Gln Pro Gln Leu Gln Thr Gln  
 610            615            620  
 Leu Gln Pro Gln Ile Gln Pro Gln Pro Gln Leu Leu Pro Val Ser Ala  
 625            630            635            640  
 Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu Ser Ala Val Ser  
 645            650            655  
 Thr Ser Ser Glu Tyr Met Gly Gly Ser Ala Ala Ile Gly Pro Ile Thr  
 660            665            670  
 Pro Ala Thr Thr Ser Ser Ile Thr Ala Ala Val Thr Ala Ser Ser Thr  
 675            680            685  
 Thr Ser Ala Val Pro Met Gly Asn Gly Val Gly Val Gly Val Gly Val  
 690            695            700  
 Gly Gly Asn Val Ser Met Tyr Ala Asn Ala Gln Thr Ala Met Ala Leu  
 705            710            715            720  
 Met Gly Val Ala Leu His Ser His Gln Glu Gln Leu Ile Gly Gly Val  
 725            730            735  
 Ala Val Lys Ser Glu His Ser Thr Thr Ala  
 740            745

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2241
- (D) OTHER INFORMATION: /product= "VpEcR"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATG CCC CCC CCG ACC GAT CTC AGC CTG GCG GAC GAG CTC CAC TTA GAC    48  
 Met Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp  
 1            5            10            15

GCG GAC GAC CTG CCG ATG CCG CAT CCG GAC CCG CTA GAC GAT TTC GAT    96  
 Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp  
 20            25            30

CTG GAC ATG TTG GGG CAC GGG GAT TCC CCG GGT CCG GGA TTT ACC CCC 144  
 Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro  
     35        40        45

CAC GAC TCC GCC CCG TAC GGC GCT CTG GAT ATG GCC GAC TTC GAG TTT 192  
 His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe  
     50        55        60

GAG CAG ATG TTT ACC GAT GCC CTT GCA ATT GAC GAG TAC CGT GGG AAG 240  
 Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly Lys  
     65        70        75        80

CTT CTA GGT ACC TCT AGA AGG ATA TCG AAT TCT ATA TCT TCA GGT CCG 288  
 Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg  
     85        90        95

GAT GAT CTC TCG CCT TCG AGC AGC TTG AAC GGA TAC TCG CGC AAC GAA 336  
 Asp Asp Leu Ser Pro Ser Ser Ser Leu Asn Gly Tyr Ser Ala Asn Glu  
     100        105        110

ACC TGC GAT CGC AAG AAG AGC AAG AAG GGA CTT GCG CCA CCG CTC CAA 384  
 Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala Pro Arg Val Gln  
     115        120        125

GAG GAG CTC TGC CTC GTT TGC GGC CAC AGC GCC TCC GCG TAC CAC TAC 432  
 Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr  
     130        135        140

AAC GCC CTC ACC TGT GAG GGC TGC AAG GGG TTC TTT CGA CCG AGC GTT 480  
 Asn Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val  
     145        150        155        160

ACG AAG AGC GCC CTC TAC TGC TGC AAG TTC GCG CGC GCC TGC GAA ATG 528  
 Thr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg Ala Cys Glu Met  
     165        170        175

GAC ATG TAC ATG AGC CGA AAG TGT CAG GAG TCC CGC CTC AAA AAG TCC 576  
 Asp Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys  
     180        185        190

CTG GCC CTC GGT ATG CCG CCG GAA TGC CTC CTC CCG GAG AAC CAA TGT 624  
 Leu Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys  
     195        200        205

GCG ATG AAG CCG CCG GAA AAG AAG GCC CAG AAG GAG AAG GAC AAA ATG 672  
 Ala Met Lys Arg Arg Glu Lys Lys Ala Gln Lys Glu Lys Asp Lys Met  
     210        215        220

ACC ACT TCG CCG AGC TCT CAG CAT GCC GCG AAT GCC AGC TTC GCC TCT 720  
 Thr Thr Ser Pro Ser Ser Gln His Gly Gly Asn Gly Ser Leu Ala Ser  
     225        230        235        240

GGT GCC GCC CAA GAC TTT GTT AAG AAG GAG ATT CTT GAC CTT ATG ACA 768  
 Gly Gly Gly Gln Asp Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr  
     245        250        255

TGC CAG CCG CCC CAG CAT GCC ACT ATT CCG CTA CTA CXT GAT GAA ATA 816  
 Cys Glu Pro Pro Gln His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile  
 260 265 270

TTG GCC AAG TGT CAA GCG CCG AAT ATA CCT TCC TTA ACC TAC AAT CAG 864  
 Leu Ala Lys Cys Gln Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln  
 275 280 285

TTG GCC GTT ATA TAC AAG TTA ATT TCG TAC CAG GAT GCG TAT GAG CAG 912  
 Leu Ala Val Ile Tyr Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln  
 290 295 300

CCA TCT GAA CAG GAT CTC AGG CGT ATA ATG ACT CAA CCC GAT GAG AAC 960  
 Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn  
 305 310 315 320

GAG AGC CAA ACG CAC GTC AGC TTT CCG CAT ATA ACC CAG ATA ACC ATA 1008  
 Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile  
 325 330 335

CTC ACG CTC CAG TTC ATT GTT CAG TTT GCT AAA GGT CTA CCA GCG TTT 1056  
 Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe  
 340 345 350

ACA AAG ATA CCC CAG CAG GAC CAG ATC ACG TTA CTA AAG GCG TCG TCG 1104  
 Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser  
 355 360 365

TCG CAG CTC ATG ATG CTC CGT ATG GCA CCA CCG TAT GAC CAC AGC TCG 1152  
 Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser  
 370 375 380

GAC TCA ATA TTC TTC CCG AAT AAT ACA TCA TAT ACG CCG GAT TGT TAC 1200  
 Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr  
 385 390 395 400

AAA ATG CCG GGA ATG GCT GAT AAC ATT GAA CAC CTC CTC CAT TTC TCG 1248  
 Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys  
 405 410 415

CCG CAA ATG TTC TCG ATG AAG CTC GAC AAC GTC GAA TAC CCG CTT CTC 1296  
 Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu  
 420 425 430

ACT GCC ATT CTC ATC TTC TCG GAC CCG CCG GCG CTC GAG AAG GCG CAA 1344  
 Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Gln  
 435 440 445

CTA CTC GAA CCG ATC CAG AGC TAC TAC ATC GAC ACG CTA CCG ATT TAT 1392  
 Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr  
 450 455 460

ATA CTC AAC CCG CAC TCG CCG GAC TCA ATG AGC CTC CTC TTC TAC CCA 1440  
 Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala  
 465 470 475 480

AAG CTC CTC TCG ATC CTC ACC GAG CTC CGT ACG CTC GGC AAC CAG AAC 1488  
 Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn  
 485 490 495

CCC GAG ATG TGT TTC TCA CTA AAG CTC AAA AAC CCG AAA CTC CCC AAG 1536  
 Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys  
 500 505 510

TTC CTC GAG GAG ATC TGG GAG GTT CAT GCC ATC CCG CCA TCG CTC CAG 1584  
 Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Gln  
 515 520 525

TGC CAC CTT CAG ATT ACC CAG GAG GAG AAC GAG CGT CTC GAG CCG GCT 1632  
 Ser His Leu Glu Ile Thr Gln Glu Glu Asn Glu Arg Leu Glu Arg Ala  
 530 535 540

GAG CGT ATC CCG GCA TCG GTT CCG GCG GCC ATT ACC GCC GCG ATT CAT 1680  
 Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp  
 545 550 555 560

TGC GAG TCT GCC TCC ACT TCG CCG GCG GCA GCC CCG GCC CAG CAT CAG 1728  
 Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala Ala Gln His Gln  
 565 570 575

CCT CAG CCT CAG CCC CAG CCC CAA CCC TCC TCC CTC ACC CAG AAC GAT 1776  
 Pro Gln Pro Gln Pro Gln Pro Gln Pro Ser Ser Leu Thr Gln Asn Asp  
 580 585 590

TCC CAG CAG CAG ACA CAG CCG CAG CTA CAA CCT CAG CTA CCA CCT CAG 1824  
 Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln Leu Pro Pro Gln  
 595 600 605

CTG CAA GGT CAA CTG CAA CCC CAG CTC CAA CCA CAG CTT CAG ACG CAA 1872  
 Leu Gln Gly Gln Leu Gln Pro Gln Leu Gln Pro Gln Leu Gln Thr Gln  
 610 615 620

CTC CAG CCA CAG ATT CAA CCA CAG CCA CAG CTC CTT CCC CTC TCC GCT 1920  
 Leu Gln Pro Gln Ile Gln Pro Gln Pro Gln Leu Leu Pro Val Ser Ala  
 625 630 635 640

CCC CTC CCC GCC TCC GTA ACC GCA CCT GGT TCC TTC TCC GCG CTC ACT 1968  
 Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu Ser Ala Val Ser  
 645 650 655

ACG AGC AGC GAA TAC ATG GGC GGA AGT CCG GCC ATA GGA CCC ATC ACG 2016  
 Thr Ser Ser Glu Tyr Met Gly Gly Ser Ala Ala Ile Gly Pro Ile Thr  
 660 665 670

CCG GCA ACC ACC AGC AGT ATC ACG GCT GCC GTT ACC GCT ACG TCC ACC 2064  
 Pro Ala Thr Thr Ser Ser Ile Thr Ala Ala Val Thr Ala Ser Ser Thr  
 675 680 685

ACA TCA CCG GTA CCG ATG GGC AAC GCA GTT GGA CTC GGT GTT GCG CTC 2112  
 Thr Ser Ala Val Pro Met Gly Asn Gly Val Gly Val Gly Val Gly Val  
 690 695 700

GGC GGC AAC CTC AGC ATG TAT GCG AAC GCG CAG ACG GCG ATG CCC TTG 2160  
 Gly Gly Asn Val Ser Met Tyr Ala Asn Ala Gln Thr Ala Met Ala Leu  
 705 710 715 720

ATG GGT GTA GCC CTC CAT TCG CAC CAA CAG CAG CTT ATC GCG GGA CTC 2208  
 Met Gly Val Ala Leu His Ser His Gln Glu Gln Leu Ile Gly Gly Val  
 725 730 735

GCG GTT AAG TCG CAG CAC TCG ACG ACT GCA TAG 2241  
 Ala Val Lys Ser Glu His Ser Thr Thr Ala  
 740 745

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 746 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp  
 1 5 10 15

Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp  
 20 25 30

Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro  
 35 40 45

His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe  
 50 55 60

Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly Lys  
 65 70 75 80

Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg  
 85 90 95

Asp Asp Leu Ser Pro Ser Ser Ser Leu Asn Gly Tyr Ser Ala Asn Glu  
 100 105 110

Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala Pro Arg Val Gln  
 115 120 125

Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr  
 130 135 140

Asn Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val  
 145 150 155 160

Thr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg Ala Cys Glu Met

165	170	175
Asp Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys		
180	185	190
Leu Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys		
195	200	205
Ala Met Lys Arg Arg Glu Lys Lys Ala Gln Lys Glu Lys Asp Lys Met		
210	215	220
Thr Thr Ser Pro Ser Ser Gln His Gly Gly Asn Gly Ser Leu Ala Ser		
225	230	235
Gly Gly Gly Gln Asp Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr		
245	250	255
Cys Glu Pro Pro Gln His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile		
260	265	270
Leu Ala Lys Cys Gln Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln		
275	280	285
Leu Ala Val Ile Tyr Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln		
290	295	300
Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn		
305	310	315
Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile		
325	330	335
Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe		
340	345	350
Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser		
355	360	365
Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser		
370	375	380
Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr		
385	390	395
Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys		
405	410	415
Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu		
420	425	430
Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Gln		
435	440	445
Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr		
450	455	460

Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala  
465            470            475            480

Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn  
485            490            495

Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys  
500            505            510

Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Gln  
515            520            525

Ser His Leu Gln Ile Thr Gln Glu Glu Asn Glu Arg Leu Glu Arg Ala  
530            535            540

Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp  
545            550            555            560

Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala Gln His Gln  
565            570            575

Pro Gln Pro Gln Pro Gln Pro Gln Pro Ser Ser Leu Thr Gln Asn Asp  
580            585            590

Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln Leu Pro Pro Gln  
595            600            605

Leu Gln Gly Gln Leu Gln Pro Gln Leu Gln Pro Gln Leu Gln Thr Gln  
610            615            620

Leu Gln Pro Gln Ile Gln Pro Gln Pro Gln Leu Leu Pro Val Ser Ala  
625            630            635            640

Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu Ser Ala Val Ser  
645            650            655

Thr Ser Ser Glu Tyr Met Gly Gly Ser Ala Ala Ile Gly Pro Ile Thr  
660            665            670

Pro Ala Thr Thr Ser Ser Ile Thr Ala Ala Val Thr Ala Ser Ser Thr  
675            680            685

Thr Ser Ala Val Pro Met Gly Asn Gly Val Gly Val Gly Val Gly Val  
690            695            700

Gly Gly Asn Val Ser Met Tyr Ala Asn Ala Gln Thr Ala Met Ala Leu  
705            710            715            720

Met Gly Val Ala Leu His Ser His Gln Glu Gln Leu Ile Gly Gly Val  
725            730            735

Ala Val Lys Ser Glu His Ser Thr Thr Ala  
740            745

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3126 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

## (ii) MOLECULE TYPE: cDNA

## (iii) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..3126  
 (D) OTHER INFORMATION: /product = "GCCR"

## (iv) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```

ATG CAC TCC AAA GAA TCA TTA ACT CCT GGT AGA GAA GAA AAC CCC AGC   48
Met Asp Ser Lys Glu Ser Leu Thr Pro Gly Arg Glu Glu Asn Pro Ser
   1       5       10      15

ACT CTC CTT GCT CAG CAG AGG CGA GAT CTC ATG GAC TTC TAT AAA ACC   96
Ser Val Leu Ala Gln Glu Arg Gly Asp Val Met Asp Phe Tyr Lys Thr
   20      25      30

CTA AGA GGA CGA GCT ACT CTC AAG GTT TCT GCG TCT TCA CCC TCA CTC   144
Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Leu
   35      40      45

GCT CTC GCT TCT CAA TCA GAC TCC AAG CAG CGA AGA CTT TTG GTT GAT   192
Ala Val Ala Ser Gln Ser Asp Ser Lys Gln Arg Arg Leu Leu Val Asp
   50      55      60

TTT CCA AAA GGC TCA CTA AGC AAT GCG CAG CAG CCA GAT CTC TCC AAA   240
Phe Pro Lys Gly Ser Val Ser Asn Ala Gln Gln Pro Asp Leu Ser Lys
   65      70      75      80

GCA GTT TCA CTC TCA ATG GGA CTC TAT ATG CGA CAG ACA GAA ACA AAA   288
Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu Thr Glu Thr Lys
   85      90      95

CTG ATG CGA AAT CAC CTC CGA TTC CCA CAG CAG GCG CAA ATC AGC CTT   336
Val Met Gly Asn Asp Leu Gly Phe Pro Gln Gln Gly Gln Ile Ser Leu
  100     105     110

TCC TCG GCG GAA ACA GAC TTA AAG CTT TTG GAA GAA AGC ATT GCA AAC   384
Ser Ser Gly Glu Thr Asp Leu Lys Leu Leu Glu Ser Ile Ala Asn
  115     120     125

CTC AAT AGC TCG ACC ACT GTT CCA GAG AAC CCC AAG ACT TCA GCA TCC   432
Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys Ser Ser Ala Ser
  130     135     140

```



ACT GCT GTG TCT GCT GCC CCC ACA GAG AAG GAG TTT CCA AAA ACT CAC 480  
 Thr Ala Val Ser Ala Ala Pro Thr Glu Lys Glu Phe Pro Lys Thr His  
 145 150 155 160

TCT GAT GTA TCT TCA GAA CAG CAA CAT TTG AAG GCC CAG ACT GCC ACC 528  
 Ser Asp Val Ser Ser Glu Gln Gln His Leu Lys Gly Gln Thr Gly Thr  
 165 170 175

AAC GGT GGC AAT GTG AAA TTG TAT ACC ACA GAG CAA AGC ACC TTT GAC 576  
 Asn Gly Gly Asn Val Lys Leu Tyr Thr Thr Asp Gln Ser Thr Phe Asp  
 180 185 190

ATT TTG CAG GAT TTG GAG TTT TCT TCT GGG TCC CCA GGT AAA CAG ACG 624  
 Ile Leu Gln Asp Leu Glu Phe Ser Ser Gly Ser Pro Gly Lys Glu Thr  
 195 200 205

AAT GAG AGT CTT TGG ACA TCA CAC CTG TTG ATA GAT CAA AAC TGT TTG 672  
 Asn Glu Ser Pro Trp Arg Ser Asp Leu Leu Ile Asp Glu Asn Cys Leu  
 210 215 220

CTT TCT CCT CTG GCC GGA GAA CAC GAT TCA TTC CTT TTG GAA GGA AAC 720  
 Leu Ser Pro Leu Ala Gly Glu Asp Asp Ser Phe Leu Leu Glu Gly Asn  
 225 230 235 240

TCC AAT GAG CAG TGC AAG CTT CTC ATT TTA CCG GAC ACT AAA CCC AAA 768  
 Ser Asn Glu Asp Cys Lys Pro Leu Ile Leu Pro Asp Thr Lys Pro Lys  
 245 250 255

ATT AAG GAT AAT GGA GAT CTC GTT TTG TCA AGC CCC AGT AAT GTA ACA 816  
 Ile Lys Asp Asn Gly Asp Leu Val Leu Ser Ser Pro Ser Asn Val Thr  
 260 265 270

CTC CCC CAA GTG AAA ACA GAA AAA CAA GAT TTG ATC GAA CTC TGC ACC 864  
 Leu Pro Gln Val Lys Thr Glu Lys Glu Asp Phe Ile Glu Leu Cys Thr  
 275 280 285

CCT GGG GTA ATT AAG CAA GAG AAA CTG GCC ACA GTT TAC TGT CAG GCA 912  
 Pro Gly Val Ile Lys Gln Glu Lys Leu Gly Thr Val Tyr Cys Gln Ala  
 290 295 300

AGC TTT CCT GGA GCA AAT ATA ATT GGT AAT AAA ATG TCT GCC ATT TCT 960  
 Ser Phe Pro Gly Ala Asn Ile Ile Gly Asn Lys Met Ser Ala Ile Ser  
 305 310 315 320

GTT CAT GCT GTG AGT ACC TCT GGA GCA CAG ATG TAC CAC TAT GAC ATG 1008  
 Val His Gly Val Ser Thr Ser Gly Gly Gln Met Tyr His Tyr Asp Met  
 325 330 335

AAT ACA GCA TCC CTT TCT CAA CAG CAG CAT CAG AAG CCT ATT TTT AAT 1056  
 Asn Thr Ala Ser Leu Ser Gln Gln Gln Asp Gln Lys Pro Ile Phe Asn  
 340 345 350

GTC ATT CCA CCA ATT CCC GTT GGT TCC GAA AAT TGC AAT AGG TGC CAA 1104  
 Val Ile Pro Pro Ile Pro Val Gly Ser Glu Asn Trp Asn Arg Cys Gln  
 355 360 365

CGA TCT GCA GAT GAC AAC TTG ACT TCT CTG GGG ACT CTG AAC TTC CCT 1152  
Gly Ser Gly Asp Asp Asn Leu Thr Ser Leu Gly Thr Leu Asn Phe Pro  
370 375 380

GGT CGA ACA GTT TTT TCT AAT GGC TAT TCA AGC CCC AGC ATG ACA CCA 1200  
Gly Arg Thr Val Phe Ser Asn Gly Tyr Ser Ser Pro Ser Met Arg Pro  
385 390 395 400

GAT CTA AGC TCT CCT CCA TCC AGC TCC TCA ACA GCA ACA ACA GGA CCA 1248  
Asp Val Ser Ser Pro Pro Ser Ser Ser Ser Thr Ala Thr Thr Gly Pro  
405 410 415

CCT CCC AGC GGC CCC CTC CAA GAG GAG CTG TCC CTG GTT TGC GGC GAC 1296  
Pro Pro Ser Gly Arg Val Gln Gln Leu Cys Leu Val Cys Gly Asp  
420 425 430

AGG GCC TCC GGC TAC CAC TAC AAC GCC CTC ACE TGT GGA TCC TGC AAG 1344  
Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys Gly Ser Cys Lys  
435 440 445

GTG TTC TTT CCA CCC AGC GTT ACC AAG AGC GCC CTC TAC TGC TGC AAG 1392  
Val Phe Phe Arg Arg Ser Val Thr Lys Ser Ala Val Tyr Cys Cys Lys  
450 455 460

TTC GGC CCC GGC TGC CAA ATG CAC ATG TAC ATG AGG CGA AAG TGT CAG 1440  
Phe Gly Arg Ala Cys Gln Met Asp Met Tyr Met Arg Arg Lys Cys Gln  
465 470 475 480

GAG TGC CCC CTC AAA AAG TGC CTC GCC CTC CCT ATG CCC CCC GAA TGC 1488  
Glu Cys Arg Leu Lys Lys Cys Leu Ala Val Gly Met Arg Pro Gln Cys  
485 490 495

GTG CTC CCC GAG AAC CAA TGT CGC ATG AAG CCC CCC GAA AAG AAG GCC 1536  
Val Val Pro Glu Asn Gln Cys Ala Met Lys Arg Arg Glu Lys Lys Ala  
500 505 510

CAG AAG CAG AAG GAC AAA ATG ACC ACT TCC CCC AGC TCT CAG CAT GCC 1584  
Gln Lys Glu Lys Asp Lys Met Thr Thr Ser Pro Ser Ser Gln His Gly  
515 520 525

GCC AAT GCC AGC TTG GCC TCT GGT GCC GGC CAA GAC TTT GTT AAG AAG 1632  
Gly Asn Gly Ser Leu Ala Ser Gly Gly Gly Gln Asp Phe Val Lys Lys  
530 535 540

GAG ATT CTT GAC CTT ATG ACA TGC GAG CCC CCC CAG CAT GCC ACT ATT 1680  
Glu Ile Leu Asp Leu Met Thr Cys Glu Pro Pro Gln His Ala Thr Ile  
545 550 555 560

CCG CTA CTA CCT GAT GAA ATA TTG GCC AAG TGT CAA GCG CGC AAT ATA 1728  
Pro Leu Leu Pro Asp Glu Ile Leu Ala Lys Cys Gln Ala Arg Asn Ile  
565 570 575

CCT TCC TTA ACC TAC AAT CAG TTG GCC GTT ATA TACAAG TTA ATT TGC 1776  
Pro Ser Leu Thr Tyr Asn Gln Leu Ala Val Ile Tyr Lys Leu Ile Trp  
580 585 590

TAC CAG GAT GGC TAT GAG CAG CCA TCT CAA GAG GAT CTC AGG CGT ATA 1824  
 Tyr Gln Asp Gly Tyr Gln Gln Pro Ser Gln Gln Asp Leu Arg Arg Ile  
 595 600 605

ATG AGT CAA CCC GAT GAG AAC GAG AGC CAA ACG GAC CTC AGC TTT CCG 1872  
 Met Ser Gln Pro Asp Gln Asn Gln Ser Gln Thr Asp Val Ser Phe Arg  
 610 615 620

CAT ATA ACC GAG ATA ACC ATA CTC ACC GTC CAG TTC ATT GTT GAG TTT 1920  
 His Ile Thr Gln Ile Thr Ile Leu Thr Val Gln Leu Ile Val Gln Phe  
 625 630 635 640

GCT AAA GGT CTA CCA GCG TTT ACA AAG ATA CCC CAG CAG GAC CAG ATC 1968  
 Ala Lys Gly Leu Pro Ala Phe Thr Lys Ile Pro Gln Gln Asp Gln Ile  
 645 650 655

ACC TTA CTA AAG GCG TCG TCG TCG CAG GTG ATG ATG CTC CCG ATG GCA 2016  
 Thr Leu Leu Lys Ala Cys Ser Ser Gln Val Met Met Leu Arg Met Ala  
 660 665 670

CGA CCG TAT GAC CAC AGC TCG GAC TCA ATA TTC TTC CCG AAT AAT AGA 2064  
 Arg Arg Tyr Asp His Ser Ser Asp Ser Ile Phe Phe Ala Asn Asn Arg  
 675 680 685

TCA TAT ACC CCG GAT TCT TAC AAA ATG GCG GGA ATG GCT GAT AAC ATT 2112  
 Ser Tyr Thr Arg Asp Ser Tyr Lys Met Ala Gly Met Ala Asp Asn Ile  
 690 695 700

GAA GAC CTC CTC CAT TTC TCG CCG CAA ATG TTC TCG ATG AAG CTC GAC 2160  
 Gln Asp Leu Leu His Phe Cys Arg Gln Met Phe Ser Met Lys Val Asp  
 705 710 715 720

AAC CTC GAA TAC GCG CTT CTC ACT GCG ATT CTC ATC TTC TCG CAC CCG 2208  
 Asn Val Gln Tyr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser Asp Arg  
 725 730 735

CCG GCG CTC GAG AAG GCG CAA CTA GTC GAA GCG ATC CAG AGC TAC TAC 2256  
 Pro Gly Leu Gln Lys Ala Gln Leu Val Gln Ala Ile Gln Ser Tyr Tyr  
 740 745 750

ATC GAC ACC CTA CCG ATT TAT ATA CTC AAC CCG CAC TCG GCG GAC TCA 2304  
 Ile Asp Thr Leu Arg Ile Tyr Ile Leu Asn Arg His Cys Gly Asp Ser  
 755 760 765

ATG AGC CTC GTC TTC TAC GCA AAG CTG CTC TCG ATC CTC ACC GAG CTC 2352  
 Met Ser Leu Val Phe Tyr Ala Lys Leu Leu Ser Ile Leu Thr Gln Leu  
 770 775 780

CGT ACC CTC GCG AAC CAG AAC GCG GAG ATG TGT TTC TCA CTA AAG CTC 2400  
 Arg Thr Leu Gly Asn Gln Asn Ala Gln Met Cys Phe Ser Leu Lys Leu  
 785 790 795 800

AAA AAC CCG AAA CTC CCG AAG TTC CTC GAG GAG ATC TCG GAC GTT CAT 2448  
 Lys Asn Arg Lys Leu Pro Lys Phe Leu Gln Gln Ile Trp Asp Val His  
 805 810 815

GCC ATC CCG CCA TCG CTC CAG TCG CAC CTT CAG ATT ACC CAG CAG CAG 2496  
 Ala Ile Pro Pro Ser Val Gln Ser His Leu Gln Ile Thr Gln Gln Gln  
 820 825 830

AAC CAG CCG CTC CAG CCG GGT CAG CCG ATG CCG CCA TCG CTT CCG CCG 2544  
 Asn Gln Arg Leu Gln Arg Ala Gln Arg Met Arg Ala Ser Val Gly Gly  
 835 840 845

GCC ATT ACC GCG GCG ATT GAT TCG CAC TCT GCG TCG ACT TCG GCG GCG 2592  
 Ala Ile Thr Ala Gly Ile Asp Cys Asp Ser Ala Ser Thr Ser Ala Ala  
 850 855 860

GCA GCG GCG GCG CAG CAT CAG CCG CCG CAG CCG CCG CAA CCG 2640  
 Ala Ala Ala Ala Gln His Gln Pro Gln Pro Gln Pro Gln Pro Gln Pro  
 865 870 875 880

TCC TCG CTC ACC CAG AAC GAT TCG CAG CAC CAG ACA CAG CCG CAG CTA 2688  
 Ser Ser Leu Thr Gln Asn Asp Ser Gln His Gln Thr Gln Pro Gln Leu  
 885 890 895

CAA CCG CAG CTA CCA CCG CAG CTC CAA GGT CAA CTC CAA CCG CAG CTC 2736  
 Gln Pro Gln Leu Pro Pro Gln Leu Gln Gly Gln Leu Gln Pro Gln Leu  
 900 905 910

CAA CCA CAG CTT CAG ACC CAA CTC CAG CCA CAG ATT CAA CCA CAG CCA 2784  
 Gln Pro Gln Leu Gln Thr Gln Leu Gln Pro Gln Ile Gln Pro Gln Pro  
 915 920 925

CAG CTC CTT CCG CTC TCG GGT CCG CTC CCG GCG TCG CTA ACC CCA CCG 2832  
 Gln Leu Leu Pro Val Ser Ala Pro Val Pro Ala Ser Val Thr Ala Pro  
 930 935 940

GGT TCG TTG TCG CCG CTC ACT ACC AGC AGC CAA TAC ATG CCG CCA ACT 2880  
 Gly Ser Leu Ser Ala Val Ser Thr Ser Ser Gln Tyr Met Gly Gly Ser  
 945 950 955 960

GCG GCG ATA GGA CCG ATC ACC CCG CCA ACC ACC AGC ACT ATC ACC GGT 2928  
 Ala Ala Ile Gly Pro Ile Thr Pro Ala Thr Thr Ser Ser Ile Thr Ala  
 965 970 975

GCG GTT ACC GGT ACC TCG ACC ACA TCA CCG CTA CCG ATG CCG AAC GGA 2976  
 Ala Val Thr Ala Ser Ser Thr Thr Ser Ala Val Pro Met Gly Asn Gly  
 980 985 990

GTT GCA CTC GGT GTT GCG GTC GCG GCG AAC GTC AGC ATG TAT CCG AAC 3024  
 Val Gly Val Gly Val Gly Val Gly Gly Asn Val Ser Met Tyr Ala Asn  
 995 1000 1005

GCG CAG ACC GCG ATG GCG TTG ATG GGT CTA GCG CTC CAT TCG CAG CAA 3072  
 Ala Gln Thr Ala Met Ala Leu Met Gly Val Ala Leu His Ser His Gln  
 1010 1015 1020

GAG CAG CTT ATC GCG GCA CTC GCG GTT AAG TCG CAG CAC TCG ACC ACT 3120  
 Gln Gln Leu Ile Gly Gly Val Ala Val Lys Ser Gln His Ser Thr Thr  
 1025 1030 1035 1040

GCA TAG  
Ala

3126

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1041 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```

Met Asp Ser Lys Gln Ser Leu Thr Pro Gly Arg Gln Gln Asn Pro Ser
 1      5      10      15

Ser Val Leu Ala Gln Gln Arg Gly Asp Val Met Asp Phe Tyr Lys Thr
 20      25      30

Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Leu
 35      40      45

Ala Val Ala Ser Gln Ser Asp Ser Lys Gln Arg Arg Leu Leu Val Asp
 50      55      60

Phe Pro Lys Gly Ser Val Ser Asn Ala Gln Gln Pro Asp Leu Ser Lys
 65      70      75      80

Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Gln Thr Glu Thr Lys
 85      90      95

Val Met Gly Asn Asp Leu Gly Phe Pro Gln Gln Gly Gln Ile Ser Leu
100      105      110

Ser Ser Gly Gln Thr Asp Leu Lys Leu Leu Gln Gln Ser Ile Ala Asn
115      120      125

Leu Asn Arg Ser Thr Ser Val Pro Gln Asn Pro Lys Ser Ser Ala Ser
130      135      140

Thr Ala Val Ser Ala Ala Pro Thr Glu Lys Gln Phe Pro Lys Thr His
145      150      155      160

Ser Asp Val Ser Ser Gln Gln Gln His Leu Lys Gly Gln Thr Gly Thr
165      170      175

Asn Gly Gly Asn Val Lys Leu Tyr Thr Thr Asp Gln Ser Thr Phe Asp
180      185      190

De Leu Gln Asp Leu Glu Phe Ser Ser Gly Ser Pro Gly Lys Glu Thr
195      200      205

```

Asn Glu Ser Pro Trp Arg Ser Asp Leu Ile Asp Glu Asn Cys Leu  
210 215 220

Leu Ser Pro Leu Ala Gly Glu Asp Asp Ser Phe Leu Leu Glu Gly Asn  
225 230 235 240

Ser Asn Glu Asp Cys Lys Pro Leu Ile Leu Pro Asp Thr Lys Pro Lys  
245 250 255

Ile Lys Asp Asn Gly Asp Leu Val Leu Ser Ser Pro Ser Asn Val Thr  
260 265 270

Leu Pro Gln Val Lys Thr Glu Lys Glu Asp Phe Ile Glu Leu Cys Thr  
275 280 285

Pro Gly Val Ile Lys Gln Glu Lys Leu Gly Thr Val Tyr Cys Gln Ala  
290 295 300

Ser Phe Pro Gly Ala Asn Ile Ile Gly Asn Lys Met Ser Ala Ile Ser  
305 310 315 320

Val His Gly Val Ser Thr Ser Gly Gly Gln Met Tyr His Tyr Asp Met  
325 330 335

Asn Thr Ala Ser Leu Ser Gln Gln Gln Asp Gln Lys Pro Ile Phe Asn  
340 345 350

Val Ile Pro Pro Ile Pro Val Gly Ser Glu Asn Trp Asn Arg Cys Gln  
355 360 365

Gly Ser Gly Asp Asp Asn Leu Thr Ser Leu Gly Thr Leu Asn Phe Pro  
370 375 380

Gly Arg Thr Val Phe Ser Asn Gly Tyr Ser Ser Pro Ser Met Arg Pro  
385 390 395 400

Asp Val Ser Ser Pro Pro Ser Ser Ser Thr Ala Thr Thr Gly Pro  
405 410 415

Pro Pro Ser Gly Arg Val Gln Glu Glu Leu Cys Leu Val Cys Gly Asp  
420 425 430

Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys Gly Ser Cys Lys  
435 440 445

Val Phe Phe Arg Arg Ser Val Thr Lys Ser Ala Val Tyr Cys Cys Lys  
450 455 460

Phe Gly Arg Ala Cys Glu Met Asp Met Tyr Met Arg Arg Lys Cys Gln  
465 470 475 480

Glu Cys Arg Leu Lys Lys Cys Leu Ala Val Gly Met Arg Pro Glu Cys  
485 490 495

Val Val Pro Glu Asn Gln Cys Ala Met Lys Arg Arg Glu Lys Lys Ala  
500 505 510

Gln Lys Glu Lys Asp Lys Met Thr Thr Ser Pro Ser Ser Gln His Gly  
515 520 525

Gly Asn Gly Ser Leu Ala Ser Gly Gly Gly Gln Asp Phe Val Lys Lys  
530 535 540

Glu Ile Leu Asp Leu Met Thr Cys Glu Pro Pro Gln His Ala Thr Ile  
545 550 555 560

Pro Leu Leu Pro Asp Glu Ile Leu Ala Lys Cys Gln Ala Arg Asn Ile  
565 570 575

Pro Ser Leu Thr Tyr Asn Gln Leu Ala Val Ile Tyr Lys Leu Ile Trp  
580 585 590

Tyr Gln Asp Gly Tyr Glu Gln Pro Ser Glu Glu Asp Leu Arg Arg Ile  
595 600 605

Met Ser Gln Pro Asp Glu Asn Glu Ser Gln Thr Asp Val Ser Phe Arg  
610 615 620

His Ile Thr Glu Ile Thr Ile Leu Thr Val Gln Leu Ile Val Glu Phe  
625 630 635 640

Ala Lys Gly Leu Pro Ala Phe Thr Lys Ile Pro Gln Glu Asp Gln Ile  
645 650 655

Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met Met Leu Arg Met Ala  
660 665 670

Arg Arg Tyr Asp His Ser Ser Asp Ser Ile Phe Phe Ala Asn Asn Arg  
675 680 685

Ser Tyr Thr Arg Asp Ser Tyr Lys Met Ala Gly Met Ala Asp Asn Ile  
690 695 700

Glu Asp Leu Leu His Phe Cys Arg Gln Met Phe Ser Met Lys Val Asp  
705 710 715 720

Asn Val Gln Tyr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser Asp Arg  
725 730 735

Pro Gly Leu Glu Lys Ala Gln Leu Val Glu Ala Ile Gln Ser Tyr Tyr  
740 745 750

Ile Asp Thr Leu Arg Ile Tyr Ile Leu Asn Arg His Cys Gly Asp Ser  
755 760 765

Met Ser Leu Val Phe Tyr Ala Lys Leu Leu Ser Ile Leu Thr Glu Leu  
770 775 780

Arg Thr Leu Gly Asn Gln Asn Ala Glu Met Cys Phe Ser Leu Lys Leu  
785 790 795 800

Lys Asn Arg Lys Leu Pro Lys Phe Leu Gln Glu Ile Trp Asp Val His  
805 810 815

Ala Ile Pro Pro Ser Val Gln Ser His Leu Gln Ile Thr Gln Glu Glu  
820 825 830

Asn Glu Arg Leu Glu Arg Ala Glu Arg Met Arg Ala Ser Val Gly Gly  
835 840 845

Ala Ile Thr Ala Gly Ile Asp Cys Asp Ser Ala Ser Thr Ser Ala Ala  
850 855 860

Ala Ala Ala Ala Gln His Gln Pro Gln Pro Gln Pro Gln Pro Gln Pro  
865 870 875 880

Ser Ser Leu Thr Gln Asn Asp Ser Gln His Gln Thr Gln Pro Gln Leu  
885 890 895

Gln Pro Gln Leu Pro Pro Gln Leu Gln Gly Gln Leu Gln Pro Gln Leu  
900 905 910

Gln Pro Gln Leu Gln Thr Gln Leu Gln Pro Gln Ile Gln Pro Gln Pro  
915 920 925

Gln Leu Leu Pro Val Ser Ala Pro Val Pro Ala Ser Val Thr Ala Pro  
930 935 940

Gly Ser Leu Ser Ala Val Ser Thr Ser Ser Glu Tyr Met Gly Gly Ser  
945 950 955 960

Ala Ala Ile Gly Pro Ile Thr Pro Ala Thr Thr Ser Ser Ile Thr Ala  
965 970 975

Ala Val Thr Ala Ser Ser Thr Thr Ser Ala Val Pro Met Gly Asn Gly  
980 985 990

Val Gly Val Gly Val Gly Val Gly Gly Asn Val Ser Met Tyr Ala Asn  
995 1000 1005

Ala Gln Thr Ala Met Ala Leu Met Gly Val Ala Leu His Ser His Gln  
1010 1015 1020

Gln Gln Leu Ile Gly Gly Val Ala Val Lys Ser Glu His Ser Thr Thr  
1025 1030 1035 1040

Ala



## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

## (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /product= "Modified Ecdysone Response Element"  
/note= "N at position 7 is 0 up to 5 nucleotides, with 1 nucleotide being especially preferred."

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

RCBNNMNTCN NCY

13

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

## (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /product= "Modified Ecdysone Response Element"  
/note= "N at position 7 can be 0 up to 5 nucleotides, with 1 nucleotide being preferred."

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

RCNNCANKNN VCY

13

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AGTGCANTGT TCT

13

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /product= "Ecdysone Response Element"  
/note= "N at position 7 can be 0 up to 5 nucleotides, with 3 nucleotides being preferred."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

RCBNNHNRGB NNM

13

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TACAACGCCC TCACCTGTGG ATCCTGCAAG GTCTTTCTTT CCACGCAGC

49

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GTACTCCCC GCGCGGCGTA TCGCGGCGG CGCTAATCG TAGCGCGCG GCA 53

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTACTCCCC GCGCGTAGG ATTAGCGCG CCGCGATAG CCGCGCGCG GCA 53

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGCTCGATCG ACAAGTGCAT TGTTCCTTGC TGA 34

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(a) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AGCTTTCACC AAGAGAAACA TGCATTGTC CATCG